RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: US|09|487,841
Source: TPW16
Date Processed by STIC: 12-22-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u>
<u>VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
   Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/487,841

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ___ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) ___. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ___ Skipped Sequences   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 ___ Skipped Sequences   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or
Response   scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ___ Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 6), No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

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 4 <110> APPLICANT: Gravel, Roy A,
 5       Rozen, Rima
 6       Leclerc, Daniel
 7       Wilson, Aaron
 8       Rosenblatt, David
10 <120> TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
11       CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
12       DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME
15 <130> FILE REFERENCE: 50004/003004
17 <140> CURRENT APPLICATION NUMBER: 09/487,841
18 <141> CURRENT FILING DATE: 2000-01-19
20 <150> PRIOR APPLICATION NUMBER: 09/371,347
21 <151> PRIOR FILING DATE: 1999-08-10
23 <150> PRIOR APPLICATION NUMBER: 09/232,028
24 <151> PRIOR FILING DATE: 1999-01-15
26 <150> PRIOR APPLICATION NUMBER: 60/071,622
27 <151> PRIOR FILING DATE: 1998-01-16
29 <160> NUMBER OF SEQ ID NOS: 61
31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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Does Not Comply
Corrected Diskette Needed
(pg.3,5-19,12,14,16)

ERRORED SEQUENCES

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315 <210> SEQ ID NO: 21
316 <211> LENGTH: 698
317 <212> TYPE: PRT
318 <213> ORGANISM: Homo sapiens
320 <400> SEQUENCE: 21
321 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
322 1               5                   10                  15
323 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
324             20                  25                  30
325 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
326         35                  40                  45
327 Glu Thr Ala Pro Leu Val Val Val Val Ser Thr Thr Gly Thr Gly Asp
328     50              55                  60
329 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
330 65                  70                  75                  80
331 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
332                 85                  90                  95
333 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
334             100                 105                 110
335 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
```

RAW SEQUENCE LISTING   DATE: 12/22/2004
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Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
336         115                 120                 125
337 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
338         130             135                 140
339 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
340 145             150                 155                 160
341 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
342             165                 170                 175
343 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
344             180                 185                 190
345 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
346         195                 200                 205
347 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
348         210             215                 220
349 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
350 225                 230                 235                 240
351 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
352             245                 250                 255
353 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
354             260                 265                 270
355 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
356         275                 280                 285
357 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
358         290                 295                 300
359 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
360 305             310                 315                 320
361 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
362             325                 330                 335
363 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
364             340                 345                 350
365 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
366         355                 360                 365
367 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
368         370             375                 380
369 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
370 385             390                 395                 400
371 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
372             405                 410                 415
373 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
374             420                 425                 430
375 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
376         435                 440                 445
377 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
378         450             455                 460
379 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
380 465             470                 475                 480
381 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
382             485                 490                 495
383 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
384         500             505                 510
```

RAW SEQUENCE LISTING   DATE: 12/22/2004
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Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
385 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
386         515             520             525
387 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
388         530             535             540
389 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
390 545             550             555             560
391 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
392         565             570             575
393 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
394         580             585             590
395 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
396         595             600             605
397 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
398         610             615             620
399 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
400 625             630             635             640
401 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
402         645             650             655
403 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
404         660             665             670
E--> 405
Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu      675                 680
    407 <210> SEQ ID NO: 22
    408 <211> LENGTH: 682
    409 <212> TYPE: PRT
    410 <213> ORGANISM: Caenorhabditis elegans
    412 <400> SEQUENCE: 22
    413 Met Thr Asp Phe Leu Ile Ala Phe Gly Ser Gln Thr Gly Gln Ala Glu
    414 1           5               10              15
    415 Thr Ile Ala Lys Ser Leu Lys Glu Lys Ala Glu Leu Ile Gly Leu Thr
    416         20              25              30
    417 Pro Arg Leu His Ala Leu Asp Glu Asn Glu Lys Lys Phe Asn Leu Asn
    418     - 35              40              45
    419 Glu Glu Lys Leu Cys Ala Ile Val Val Ser Ser Thr Gly Asp Gly Asp
    420     50              55              60
    421 Ala Pro Asp Asn Cys Ala Arg Phe Val Arg Arg Ile Asn Arg Asn Ser
    422 65              70              75              80
    423 Leu Glu Asn Glu Tyr Leu Lys Asn Leu Asp Tyr Val Leu Leu Gly Leu
    424             85              90              95
    425 Gly Asp Ser Asn Tyr Ser Ser Tyr Gln Thr Ile Pro Arg Lys Ile Asp
    426         100             105             110
    427 Lys Gln Leu Thr Ala Leu Gly Ala Asn Arg Leu Phe Asp Arg Ala Glu
    428         115             120             125
    429 Ala Asp Asp Gln Val Gly Leu Glu Leu Glu Val Glu Pro Trp Ile Glu
    430     - 130             135             140
    431 Lys Phe Phe Ala Thr Leu Ala Ser Arg Phe Asp Ile Ser Ala Asp Lys
    432 145             150             155             160
    433 Met Asn Ala Ile Thr Glu Ser Ser Asn Leu Lys Leu Asn Gln Val Lys
    434         165             170             175
    435 Thr Glu Glu Glu Lys Lys Ala Leu Leu Gln Lys Arg Ile Glu Asp Glu
```

```
436              180                185                190
437 Glu Ser Asp Asp Glu Gly Arg Gly Arg Val Ile Gly Ile Asp Met Leu
438          195                200                205
439 Ile Pro Glu His Tyr Asp Tyr Pro Glu Ile Ser Leu Leu Lys Gly Ser
440      210                215                220
441 Gln Thr Leu Ser Asn Asp Glu Asn Leu Arg Val Pro Ile Ala Pro Gln
442 225                230                235                240
443 Pro Phe Ile Val Ser Ser Val Ser Asn Arg Lys Leu Pro Glu Asp Thr
444              245                250                255
445 Lys Leu Glu Trp Gln Asn Leu Cys Lys Met Pro Gly Val Val Thr Lys
446          260                265                270
447 Pro Phe Glu Val Leu Val Val Ser Ala Glu Phe Val Thr Asp Pro Phe
448          275                280                285
449 Ser Lys Lys Ile Lys Thr Lys Arg Met Ile Thr Val Asp Phe Gly Asp
450      290                295                300
451 His Ala Ala Glu Leu Gln Tyr Glu Pro Gly Asp Ala Ile Tyr Phe Cys
452 305                310                315                320
453 Val Pro Asn Pro Ala Leu Glu Val Asn Phe Ile Leu Lys Arg Cys Gly
454 ·              325                330                335
455 Val Leu Asp Ile Ala Asp Gln Gln Cys Glu Leu Ser Ile Asn Pro Lys
456          340                345                350
457 Thr Glu Lys Ile Asn Ala Gln Ile Pro Gly His Val His Lys Ile Thr
458          355                360                365
459 Thr Leu Arg His Met Phe Thr Thr Cys Leu Asp Ile Arg Arg Ala Pro
460      370                375                380
461 Gly Arg Pro Leu Ile Arg Val Leu Ala Glu Ser Thr Ser Asp Pro Asn
462 385                390                395                400
463 Glu Lys Arg Arg Leu Leu Glu Leu Cys Ser Ala Gln Gly Met Lys Asp
464              405                410                415
465 Phe Thr Asp Phe Val Arg Thr Pro Gly Leu Ser Leu Ala Asp Met Leu
466          420                425                430
467 Phe Ala Phe Pro Asn Val Lys Pro Pro Val Asp Arg Leu Ile Glu Leu
468          435                440                445
469 Leu Pro Arg Leu Ile Pro Arg Pro Tyr Ser Met Ser Ser Tyr Glu Asn
470      450                455                460
471 Arg Lys Ala Arg Leu Ile Tyr Ser Glu Met Glu Phe Pro Ala Thr Asp
472 465                470                475                480
473 Gly Arg Arg His Ser Arg Lys Gly Leu Ala Thr Asp Trp Leu Asn Ser
474 .              485                490                495
475 Leu Arg Ile Gly Asp Lys Val Gln Val Leu Gly Lys Glu Pro Ala Arg
476          500                505                510
477 Phe Arg Leu Pro Pro Leu Gly Met Thr Lys Asn Ser Ala Gly Lys Leu
478          515                520                525
479 Pro Leu Leu Met Val Gly Pro Gly Thr Gly Val Ser Val Phe Leu Ser
480      530                535                540
481 Phe Leu His Phe Leu Arg Lys Leu Lys Gln Asp Ser Pro Ser Asp Phe
482 545                550                555                560
483 Val Asp Val Pro Arg Val Leu Phe Phe Gly Cys Arg Asp Ser Ser Val
484              565                570                575
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RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
485 Asp Ala Ile Tyr Met Ser Glu Leu Glu Met Phe Val Ser Glu Gly Ile
486         580             585             590
487 Leu Thr Asp Leu Ile Ile Cys Glu Ser Glu Gln Lys Gly Glu Arg Val
488         595             600             605
489 Gln Asp Gly Leu Arg Lys Tyr Leu Asp Lys Val Leu Pro Phe Leu Thr
490     610             615             620
491 Ala Ser Thr Glu Ser Lys Ile Phe Ile Cys Gly Asp Ala Lys Gly Met
492 625             630             635             640
493 Ser Lys Asp Val Trp Gln Cys Phe Ser Asp Ile Val Ala Ser Asp Gln
494         645             650             655
```

E--> 495
Gly Ile Pro Asp Leu Glu Ala Lys Lys Lys Leu Met Asp Leu Lys Lys   660
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    497 <210> SEQ ID NO: 23
    498 <211> LENGTH: 677
    499 <212> TYPE: PRT
    500 <213> ORGANISM: Homo sapiens
    502 <400> SEQUENCE: 23
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E--> 503 **Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val**
```
    504 1               5               10              15
    505 Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser
    506         20              25              30
    507 Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys
    508         35              40              45
    509 Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val
    510     50              55              60
    511 Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile
    512 65              70              75              80
    513 Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn
    514             85              90              95
    515 Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala
    516         100             105             110
    517 Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile
    518         115             120             125
    519 Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp
    520     130             135             140
    521 Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp
    522 145             150             155             160
    523 Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys
    524             165             170             175
    525 Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu
    526             180             185             190
    527 Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp
    528         195             200             205
    529 Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp
    530     210             215             220
    531 Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser
    532 225             230             235             240
    533 Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala
    534             245             250             255
    535 Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln
```

```
536              260              265              270
537 Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr
538          275              280              285
539 Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu
540      290              295              300
541 Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val
542 305              310              315              320
543 Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys
544              325              330              335
545 Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp
546          340              345              350
547 Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg
548      355              360              365
549 Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn
550      370              375              380
551 Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu
552 385              390              395              400
553 Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr
554          405              410              415
555 Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln
556          420              425              430
557 Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu
558          435              440              445
559 Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val
560      450              455              460
561 His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr
562 465              470              475              480
563 Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala
564          485              490              495
565 Lys Glu Pro Val Gly Glu Asn Gly Gly Arg Ala Leu Val Pro Met Phe
566          500              505              510
567 Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val
568      515              520              525
569 Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile
570      530              535              540
571 Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr
572 545              550              555              560
573 Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg
574          565              570              575
575 Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn
576          580              585              590
577 Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu
578      595              600              605
579 Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala
580      610              615              620
581 His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln
582 625              630              635              640
583 Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala
E--> 584
         645              650              655    Gln Ala Val Asp Tyr Ile Lys Lys
```

```
RAW SEQUENCE LISTING              DATE: 12/22/2004
PATENT APPLICATION:  US/09/487,841    TIME: 15:09:45

        Input Set : A:\seqlist.txt
        Output Set: N:\CRF4\12222004\I487841.raw
```

✓ SAME errors

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    648 <210> SEQ ID NO: 25
    649 <211> LENGTH: 18
    650 <212> TYPE: PRT
    651 <213> ORGANISM: Homo sapiens
    653 <400> SEQUENCE: 25
E--> 654
Gly Ala Met Trp Leu Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr 1                    5
    656 <210> SEQ ID NO: 26
    657 <211> LENGTH: 18
    658 <212> TYPE: PRT
    659 <213> ORGANISM: Homo sapiens
    661 <400> SEQUENCE: 26
E--> 662
Gly Glu Thr Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr 1                    5
    664 <210> SEQ ID NO: 27
    665 <211> LENGTH: 18
    666 <212> TYPE: PRT
    667 <213> ORGANISM: Oryctolagus cuniculus
    669 <400> SEQUENCE: 27
E--> 670
Gly Glu Thr Leu Leu Tyr Tyr Gly Cys Arg Arg Ala Ala Glu Asp Tyr 1                    5
    672 <210> SEQ ID NO: 28
    673 <211> LENGTH: 18
    674 <212> TYPE: PRT
    675 <213> ORGANISM: Drosophila melanogaster
    677 <400> SEQUENCE: 28
E--> 678
Gly Glu Ser Ile Leu Tyr Phe Gly Cys Arg Lys Arg Ser Glu Asp Tyr 1                    5
    680 <210> SEQ ID NO: 29
    681 <211> LENGTH: 18
    682 <212> TYPE: PRT
    683 <213> ORGANISM: Vigna radiata
    685 <400> SEQUENCE: 29
E--> 686
Gly Pro Ala Leu Leu Phe Phe Gly Cys Arg Asn Arg Gln Met Asp Phe 1                    5
    688 <210> SEQ ID NO: 30
    689 <211> LENGTH: 18
    690 <212> TYPE: PRT
    691 <213> ORGANISM: Aspergillus niger
    693 <400> SEQUENCE: 30
E--> 694
Gly Pro Thr Val Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe 1                    5
    696 <210> SEQ ID NO: 31
    697 <211> LENGTH: 18
    698 <212> TYPE: PRT
    699 <213> ORGANISM: Homo sapiens
    701 <400> SEQUENCE: 31
E--> 702
Cys Pro Met Val Leu Val Phe Gly Cys Arg Gln Ser Lys Ile Asp His 1                    5
    704 <210> SEQ ID NO: 32
    705 <211> LENGTH: 18
    706 <212> TYPE: PRT
    707 <213> ORGANISM: Homo sapiens
```

See item # 1 on error summary sheet.

```
    709 <400> SEQUENCE: 32
E--> 710
Gly Arg Met Thr Leu Val Phe Gly Cys Arg Arg Pro Asp Glu Asp His 1                    5
    712 <210> SEQ ID NO: 33
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SAme
erron

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
     713 <211> LENGTH: 18
     714 <212> TYPE: PRT
     715 <213> ORGANISM: Homo sapiens
     717 <400> SEQUENCE: 33
E--> 718
Thr Pro Met Thr Leu Val Phe Gly Cys Arg Cys Ser Gln Leu Asp His 1                    5
     720 <210> SEQ ID NO: 34
     721 <211> LENGTH: 18
     722 <212> TYPE: PRT
     723 <213> ORGANISM: Oryctolagus cuniculus
     725 <400> SEQUENCE: 34
E--> 726
Gly Arg Met Thr Leu Val Phe Gly Cys Arg His Pro Glu Glu Asp His 1                    5
     728 <210> SEQ ID NO: 35
     729 <211> LENGTH: 18
     730 <212> TYPE: PRT
     731 <213> ORGANISM: Gallus gallus
     733 <400> SEQUENCE: 35
E--> 734
Gly Asp Met Ile Leu Leu Phe Gly Cys Arg His Pro Asp Met Asp His 1                    5
     736 <210> SEQ ID NO: 36
     737 <211> LENGTH: 18
     738 <212> TYPE: PRT
     739 <213> ORGANISM: Escherichia coli
     741 <400> SEQUENCE: 36
E--> 742
Gly Lys Asn Trp Leu Phe Phe Gly Asn Pro His Phe Thr Glu Asp Phe 1                    5
     744 <210> SEQ ID NO: 37
     745 <211> LENGTH: 18
     746 <212> TYPE: PRT
     747 <213> ORGANISM: Saccharomyces cerevisiae
     749 <400> SEQUENCE: 37
E--> 750
Gly Glu Val Phe Leu Tyr Leu Gly Ser Arg His Lys Arg Glu Glu Tyr 1                    5
     752 <210> SEQ ID NO: 38
     753 <211> LENGTH: 18
     754 <212> TYPE: PRT
     755 <213> ORGANISM: Thiocapsa roseopersicina
     757 <400> SEQUENCE: 38
E--> 758
Gly Arg Asn Trp Leu Ile Phe Gly Asn Arg His Phe His Arg Asp Phe 1                    5
     760 <210> SEQ ID NO: 39
     761 <211> LENGTH: 19
     762 <212> TYPE: PRT
     763 <213> ORGANISM: Pisum sativum
     765 <400> SEQUENCE: 39
E--> 766
Gly Leu Ala Trp Leu Phe Leu Gly Val Ala Asn Val Asp Ser Leu Leu 1                    5
     768 <210> SEQ ID NO: 40
     769 <211> LENGTH: 18
     770 <212> TYPE: PRT
     771 <213> ORGANISM: Spinacia oleracea
     773 <400> SEQUENCE: 40
```

Same errors

See item # 1 on = error summary sheet.

E--> 774
Gly Leu Ala Trp Leu Phe Leu Gly Val Pro Thr Ser Ser Ser Leu L u l
    818 <210> SEQ ID NO: 42
    819 <211> LENGTH: 698

Same error 5

```
820 <212> TYPE: PRT
821 <213> ORGANISM: Homo sapiens
823 <400> SEQUENCE: 42
824 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
825 1               5                   10                  15
826 Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
827             20                  25                  30
828 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
829         35                  40                  45
830 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
831     50                  55                  60
832 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
833 65                  70                  75                  80
834 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
835             85                  90                  95
836 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
837             100                 105                 110
838 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
839         115                 120                 125
840 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
841     130                 135                 140
842 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
843 145                 150                 155                 160
844 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
845             165                 170                 175
846 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
847             180                 185                 190
848 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
849         195                 200                 205
850 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
851     210                 215                 220
852 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
853 225                 230                 235                 240
854 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
855             245                 250                 255
856 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
857         260                 265                 270
858 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
859         275                 280                 285
860 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
861     290                 295                 300
862 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
863 305                 310                 315                 320
864 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
865             325                 330                 335
866 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
867             340                 345                 350
868 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
869         355                 360                 365.
```

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
870 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
871     370                 375                 380
872 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
873 385             390                 395                 400
874 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
875             405                 410                 415
876 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
877             420                 425                 430
878 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
879         435                 440                 445
880 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
881     450                 455                 460
882 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
883 465             470                 475                 480
884 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
885             485                 490                 495
886 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
887         500                 505                 510
888 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
889     515                 520                 525
890 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
891     530                 535                 540
892 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
893 545             550                 555                 560
894 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
895             565                 570                 575
896 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
897         580                 585                 590
898 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
899         595                 600                 605
900 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
901     610                 615                 620
902 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
903 625             630                 635                 640
904 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
905             645                 650                 655
906 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
907         660                 665                 670
E--> 908
Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu    675                              680
952 <210> SEQ ID NO: 44
953 <211> LENGTH: 698
954 <212> TYPE: PRT
955 <213> ORGANISM: Homo sapiens
957 <400> SEQUENCE: 44
958 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
959 1               5                 10                  15
960 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
961             20                  25                  30
962 Ala Asp Leu His Thr Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
```

963		35				40					45			
964	Glu	Thr	Ala	Pro	Leu	Val	Val	Val	Val	Ser	Thr	Thr	Gly	Thr	Gly	Asp
965		50				55					60			
966	Pro	Pro	Asp	Thr	Ala	Arg	Lys	Phe	Val	Lys	Glu	Ile	Gln	Asn	Gln	Thr
967	65				70				75					80
968	Leu	Pro	Val	Asp	Phe	Phe	Ala	His	Leu	Arg	Tyr	Gly	Leu	Leu	Gly	Leu
969				85				90				95		
970	Gly	Asp	Ser	Glu	Tyr	Thr	Tyr	Phe	Cys	Asn	Gly	Gly	Lys	Ile	Ile	Asp
971			100				105				110			
972	Lys	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	His	Phe	Tyr	Asp	Thr	Gly	His
973		115				120				125				
974	Ala	Asp	Asp	Cys	Val	Gly	Leu	Glu	Leu	Val	Val	Glu	Pro	Trp	Ile	Ala
975		130				135				140				
976	Gly	Leu	Trp	Pro	Ala	Leu	Arg	Lys	His	Phe	Arg	Ser	Ser	Arg	Gly	Gln
977	145				150				155					160
978	Glu	Glu	Ile	Ser	Gly	Ala	Leu	Pro	Val	Ala	Ser	Pro	Ala	Ser	Leu	Arg
979			165				170				175			
980	Thr	Asp	Leu	Val	Lys	Ser	Glu	Leu	Leu	His	Ile	Glu	Ser	Gln	Val	Glu
981			180				185				190			
982	Leu	Leu	Arg	Phe	Asp	Asp	Ser	Gly	Arg	Lys	Asp	Ser	Glu	Val	Leu	Lys
983		195				200				205				
984	Gln	Asn	Ala	Val	Asn	Ser	Asn	Gln	Ser	Asn	Val	Val	Ile	Glu	Asp	Phe
985		210				215				220				
986	Glu	Ser	Ser	Leu	Thr	Arg	Ser	Val	Pro	Pro	Leu	Ser	Gln	Ala	Ser	Leu
987	225				230				235					240
988	Asn	Ile	Pro	Gly	Leu	Pro	Pro	Glu	Tyr	Leu	Gln	Val	His	Leu	Gln	Glu
989			245				250				255			
990	Ser	Leu	Gly	Gln	Glu	Glu	Ser	Gln	Val	Ser	Val	Thr	Ser	Ala	Asp	Pro
991			260				265				270			
992	Val	Phe	Gln	Val	Pro	Ile	Ser	Lys	Ala	Val	Gln	Leu	Thr	Thr	Asn	Asp
993		275				280				285				
994	Ala	Ile	Lys	Thr	Thr	Leu	Leu	Val	Glu	Leu	Asp	Ile	Ser	Asn	Thr	Asp
995		290				295				300				
996	Phe	Ser	Tyr	Gln	Pro	Gly	Asp	Ala	Phe	Ser	Val	Ile	Cys	Pro	Asn	Ser
997	305				310				315					320
998	Asp	Ser	Glu	Val	Gln	Ser	Leu	Leu	Gln	Arg	Leu	Gln	Leu	Glu	Asp	Lys
999			325				330				335			
1000	Arg	Glu	His	Cys	Val	Leu	Leu	Lys	Ile	Lys	Ala	Asp	Thr	Lys	Lys	Lys
1001			340				345				350			
1002	Gly	Ala	Thr	Leu	Pro	Gln	His	Ile	Pro	Ala	Gly	Cys	Ser	Leu	Gln	Phe
1003			355				360				365			
1004	Ile	Phe	Thr	Trp	Cys	Leu	Glu	Ile	Arg	Ala	Ile	Pro	Lys	Lys	Ala	Phe
1005		370				375				380				
1006	Leu	Arg	Ala	Leu	Val	Asp	Tyr	Thr	Ser	Asp	Ser	Ala	Glu	Lys	Arg	Arg
1007	385				390				395					400
1008	Leu	Gln	Glu	Leu	Cys	Ser	Lys	Gln	Gly	Ala	Ala	Asp	Tyr	Ser	Arg	Phe
1009			405				410				415			
1010	Val	Arg	Asp	Ala	Cys	Ala	Cys	Leu	Leu	Asp	Leu	Leu	Leu	Ala	Phe	Pro
1011			420				425				430			

```
1012 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
1013         435             440             445
1014 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
1015     450             455             460
1016 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
1017 465             470             475             480
1018 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
1019             485             490             495
1020 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
1021         500             505             510
1022 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
1023         515             520             525
1024 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
1025     530             535             540
1026 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
1027 545             550             555             560
1028 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
1029             565             570             575
1030 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
1031         580             585             590
1032 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
1033         595             600             605
1034 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
1035     610             615             620
1036 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
1037 625             630             635             640
1038 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
1039             645             650             655
1040 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
1041         660             665             670
E--> 1042
Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu          675          680
1086 <210> SEQ ID NO: 46
1087 <211> LENGTH: 697
1088 <212> TYPE: PRT
1089 <213> ORGANISM: Homo sapiens
1091 <400> SEQUENCE: 46
1092 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
1093 1           5               10              15
1094 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
1095             20              25              30
1096 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
1097         35              40              45
1098 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
1099     50              55              60
1100 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
1101 65              70              75              80
1102 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
1103             85              90              95
1104 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
```

Same error (handwritten annotation)

```
1105              100                105                110
1106 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
1107          115                120                125
1108 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
1109      130                135                140
1110 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
1111 145                150                155                160
1112 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
1113                  165                170                175
1114 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
1115          180                185                190
1116 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
1117          195                200                205
1118 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
1119      210                215                220
1120 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
1121 225                230                235                240
1122 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
1123                  245                250                255
1124 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
1125          260                265                270
1126 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
1127          275                280                285
1128 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
1129      290                295                300
1130 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
1131 305                310                315                320
1132 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
1133                  325                330                335
1134 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
1135              340                345                350
1136 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
1137          355                360                365
1138 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
1139      370                375                380
1140 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
1141 385                390                395                400
1142 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
1143                  405                410                415
1144 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
1145          420                425                430
1146 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
1147          435                440                445
1148 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
1149      450                455                460
1150 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
1151 465                470                475                480
1152 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
1153                  485                490                495
```

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
1154 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
1155            500                 505                 510
1156 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
1157            515                 520                 525
1158 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
1159       530                 535                 540
1160 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
1161 545                 550                 555                 560
1162 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Phe
1163            565                 570                 575
1164 Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu Leu
1165            580                 585                 590
1166 Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser Phe
1167            595                 600                 605
1168 Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr Val
1169       610                 615                 620
1170 Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu Leu
1171 625                 630                 635                 640
1172 Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met Ala
1173            645                 650                 655
1174 Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val Gly
1175       660                 665                 670
E--> 1176
Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu Glu        675                    680
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:46

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:21; Line(s) 405
Seq#:22; Line(s) 495
Seq#:23; Line(s) 584
Seq#:25; Line(s) 654
Seq#:26; Line(s) 662
Seq#:27; Line(s) 670
Seq#:28; Line(s) 678
Seq#:29; Line(s) 686
Seq#:30; Line(s) 694
Seq#:31; Line(s) 702
Seq#:32; Line(s) 710
Seq#:33; Line(s) 718
Seq#:34; Line(s) 726
Seq#:35; Line(s) 734
Seq#:36; Line(s) 742
Seq#:37; Line(s) 750
Seq#:38; Line(s) 758
Seq#:39; Line(s) 766
Seq#:40; Line(s) 774
Seq#:42; Line(s) 908
Seq#:44; Line(s) 1042
Seq#:46; Line(s) 1176

VERIFICATION SUMMARY   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:46

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\12222004\I487841.raw**

```
L:405 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:21
L:495 M:252 E: No. of Seq. differs, <211> LENGTH:Input:682 Found:656 SEQ:22
L:584 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:23
L:584 M:252 E: No. of Seq. differs, <211> LENGTH:Input:677 Found:656 SEQ:23
L:654 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:662 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:670 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:678 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:686 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:694 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:702 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:710 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:718 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:726 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:734 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:742 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:750 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:758 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:766 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:774 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:908 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:42
L:1042 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:44
L:1176 M:252 E: No. of Seq. differs, <211> LENGTH:Input:697 Found:672 SEQ:46
```